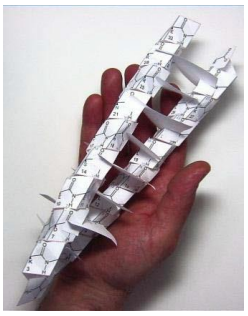
Molecular origami for biochemistry: Paper models of proteins, carbohydrates, and nucleic acids



Charles Abrams, Department of Physical Science & Engineering,
Truman College 1145 W Wilson Ave, Chicago IL 60640
cabrams@ccc.edu

Chemistry and biochemistry students study the structures of small molecules with plastic model kits, but they cannot easily use the same kits to build models of proteins, carbohydrates, or nucleic acids because of the size and complexity of those important molecules. Several solutions to this problem have been developed, but none provide the combination of precision, accuracy, ease of construction, and affordability of a plastic model kit. This work presents a set of paper models that provide all of these features. All molecules are represented in the skeletal structure format which students learn in organic chemistry. Printed lines guide cutting and folding, while numbers show where to glue or tape.

Students in Organic Chemistry II and Survey of Organic and Biochemistry have built accurate paper models of some important proteins, well beyond the relatively simple alpha helix and beta sheet. Advanced models illustrate tertiary and quaternary interactions, including the hydrophobic interactions in a Rossman fold, leucine zipper, or the collagen triple helix. A comparison between C-alpha distances in the paper models and the PDB files demonstrates that the models are accurate to an average of 5%. Comparison between models built by different students reveals excellent precision among correctly built models, and misunderstandings which provide opportunities for learning.

Models of carbohydrates clarify the intra- and intermolecular hydrogen bonding in cellulose, amylose V, amylopectin, cyclodextrins, and chitin. A model of heparin shows the large number of sulfate groups and their attachment points, and encourages students to make a detailed comparison to oversulfated chondroitin, an infamous contaminant in heparin that caused adverse reactions in patients.

A model of a DNA oligomer featuring the sequence-specific steric and hydrogen bonding environment in the major and minor grooves can also be constructed by students. The selective binding of the antibiotic netropsin to AT-rich sequences in the minor groove is explained by a model of this interaction.

All models can be made on the same scale, so it is readily apparent that an alpha helix may fit into the DNA major groove, for example. Thus, using a sophisticated paper model, groups of students built and studied the sequence-specific interaction between the leucine zipper GCN4 basic domain and the ATF/CREB site of DNA (PDB ID:2DGC).

The models have been used as lab activities, homework, or extra credit assignments and helped students make connections between structural diagrams, three-dimensional models, and interactions between biological macromolecules. Examples of student built models will be shared, and the advantages and disadvantages of this type of manipulative will be discussed.